GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 07:49:48 ; Search time 1.01497 Seconds
                        (without alignments)
                        3.508 Million cell updates/sec

Title: US-10-646-950-5
Perfect score: 373
Sequence: 1 tttgggagtcgccccatttca

Scoring table:

       IDENTITY_NUC
       Gapop 10.0 , Gapext 0.5

Database :

       US10646950_1_3.seq:*

Post-processing: Minimum Match 0%
               Maximum Match 100%
               listing first 2 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 4

Searched: 2 seqs, 4773 residues

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	30.5	8.2	2948	1	US-10-646-950-3	Sequence 3, Appli
2	16.4	4.4	1825	1	US-10-646-950-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-3
; Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)

Query Match   8.2%; Score 30.5; DB 1; Length 2948;
Best Local Similarity 49.8%; Pred. No. 0;

                         Matches 102; Conservative 0; Mismatches 100; Indels 3; Gaps 1;

Qy   1 TTTGGGAGTCGCGCCCATTTCACCCACATTATTGAGCAGCTGCGGTTCCGCGGTGCTTAT 60
         |||||||| ||| ||||||||||||| |||||||| ||||| ||||||| ||||||| |||||
Db   1568 TTTGGGACTTGCGCCACGCACACACTGCTTATTGAGCAATTACAGGAAGGCTCCATGCAACT 1627

Qy   61 GGAAGTATCTTCGTTGTCTGCAGCGTTCCAGTTCTCCTACACCGCTGTCTTCGGTGCTTAT 120
         |||||||| ||||||||| ||||||||| ||||| |||||||||||||||||||||| ||||
Db 1628 GTTTCCATTCGCTGACAACATGCTTCCAAATTTATACACAACACTTTTTGGAGGGTTA 1687

Qy   121 ACAGCTTTCCTCCTTCATCCGCACA--GGACACCTGATTAGGGCCCGGTTCTCTGCCACTCT 177
        |||||| ||||| || |||||| || |||| ||||||||||||||||||||||| ||||
Db 1688 ACCAAGTTTGTTATTCGTAAGAACAGGCGGGAACCTATGGTGCTGCATAAATCCTGCATGCC 1747

Qy   178 TTCTGCAACTACATGGGGCTTCCCTG 202
        |||| ||| ||||||||||| |||
Db 1748 CTTTGCAATATCATGGGGGTTTCCTG 1772

RESULT 2
US-10-646-950-1
; Sequence 1, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)

Query Match   4.4%; Score 16.4; DB 1; Length 1825;
Best Local Similarity 45.4%; Pred. No. 0;
Matches 59; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy   98 ACACCGCTGTCTTCGGTGCTTATACAGCTTTCCTCCTTCATCCGCACAGGACACCTGATAG 157
        |||| ||||| |||| ||| |||| ||||| |||||||||| ||||||| ||||||
Db   356 AGACGATTCTCGACCATCCTAATATCCGTGGAAATTAAATCATTTCTGGGTTCTCGATTG 415

Qy   158 GGCCGGTTCTCTGCCACTCTTCTTCTGCAACTACATGGGCTTCCCTGAGTGTGTTCAGCCC 217
        || ||||||| ||| ||||| |||||||| ||||||||||||| ||| |||||||
Db   416 CCCAATTTTCTTTCGAATCTTACTTGACGTACAGACAGTACCAGAGAGCTACTCGAAACAA 475

Qy   218 TGGAGGCATCC 227
        || |||||||
Db   476 AGTTGCCACC 485

Search completed: April 18, 2006, 07:49:50
Job time : 1.01497 secs

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OM nucleic - nucleic search, using sw model

Run on: April 18, 2006, 07:49:48 ; Search time 0.985034 Seconds
                        (without alignments)
                        3.508 Million cell updates/sec

Title:
Perfect score: 358
Sequence: US-10-646-950-6
1 cattattagccaagatgaatt...........gagagacttcaagctttgaa 362

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 4773 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 2 summaries

Database : US10646950
US10646950_1_3.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	33.7	9.4	1825	1	US-10-646-950-1	Sequence 1, Appli
2	24.4	6.8	2948	1	US-10-646-950-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-1
Sequence 1, Application US/10646950
GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)
US-10-646-950-1

Query Match 9.4%; Score 33.7; DB 1; Length 1825;
Best Local Similarity 55.2%; Pred. No. 0; Mismatches 68; Indels 1; Gaps 1;
Matches 85; Conservative 0; Conservative 0;

Qy   196 TGAGTTTCAAGCTGATGCAT-TGCCAAGAAACTTGGGAAGGCGTAAAGACTTATATTCTGC 254
           ||| ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   1509 TGAATATCAAGCTGATGCTTATGCTAAAAAAATTGGGCTACAAGCAAAAATCTATGTAGGGC 1568

Qy   255 TTTAATCAAACTTAACAAAAGATAACTTGGGATTCCCTGGTTCTGACTGGTTGTTCTCAAT 314
           |||||||| || ||| ||||| ||||| ||||||||||||||||||||||
Db   1569 TCTAATTGATCTACAAAATCAAAAAACCTTTCCACCATGAAAGTAGATCCTCTGTATTCTAG 1628

Qy   315 GTGGCATTATTCTCATCCTCCACTGCTAGAGAGA 348

Db   1629 CTATCATTATTCCCATCCAACTCTAGCTGAAAGA 1662

RESULT 2
US-10-646-950-3/c
Sequence 3, Application US/10646950
GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)
US-10-646-950-3

Query Match 6.8%; Score 24.4; DB 1; Length 2948;
Best Local Similarity 46.7%; Pred. No. 0; Mismatches 80; Indels 0; Gaps 0;
Matches 70; Conservative 0;

Qy   27   TGTGTTTTTTTTTTTTTATTTGCTGTATTAATTGGTCGAAAGGGAGCGTTTTTGCTGCANTTGGTT 86
           || |||| ||| | ||||| || |||| || ||| ||| ||| |||||||| | |||
Db   2862 TATATTTTGTTAAAGTATCTTGTACAAGCTCTAGGAAAATTATCAGGCTTAAACGTTAGGGTG 2803

Qy   87   TTTATGTNTAGGCCAACCCACTNTTATTCGGACTANTGNTCATCTTCCAGTTTATTTTTCAC 146
           ||||||| ||||| || || ||| ||| || ||||| ||| |||||
Db   2802 TTGATTGGCGGGAACCCATAATAAGTTTTTCTTTAATACGTTAGCATTAAATTCCTGA 2743

Qy   147 CTTACAATGNGGTNTTCTNTTCTTTTTTGCCTAA 176
           || ||||||| | | ||||||| ||||
Db   2742 TCGAGAGTGAACACCTTTTTTTATACCTAA 2713

Search completed: April 18, 2006, 07:49:50
Job time : 0.985034 secs

From:	Ramirez, Delia
Sent:	Monday, April 10, 2006 1:36 PM
To:	Jarrell, Noble
Subject:	10/646950

Hi,
I would like to request the following alignments:

1. SEQ ID NO:5 against SEQ ID NO:2 and 4
2. SEQ ID NO:6 against SEQ ID NO:2 and 4
3. SEQ ID NO:5 against SEQ ID NO:6
4. SEQ ID NO:5 and 6 against SEQ ID NO:1
5. SEQ ID NO:5 and 6 against SEQ ID NO:3
6. SEQ ID NO:1 and 3 against SEQ ID NO:2 and 4

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

1

Best Local Similarity: 36.4%
Query Match: 9.9%
DB: 1

Mismatches: 39
Indels: 6
Gaps: 3

US-10-646-950-4 (1-315) x US-10-646-950-5 (1-373)

```
Qy   190 PheGlyLeuAlaHisAlaHisAlaTyrGluGlnLeuGlnGlyGlySerMetThrThr 209
             |||||||||||       ||||||||        |:::
Db     1 TTTGGAGTCGCCCATTTCACCACAATTATTGAGCAGCTGGGTTCCGCCAGAGCAGTGTG 60

Qy   210 ValSerIleLeuLeuThrThrCysPheGlnIleLeuLeuTyrThrThrLeuPheGlyLeu 229
             :::          |||||||       |||||||
Db    61 GGAAGTATCTTCGTGTCTGCAGCGGTTCTCCTACACCGCTGTCTTCGGTGCTTAT 120

Qy   230 ThrLysPheValArgThrGlyGlyAsnLeuTrpCysPheIlelleIleLeuHisAla 249
             |||||||       |||       |||||||
Db   121 ACAGCTTTCCTCTTCATCGCCA---GGACACTGATAGGGCGCGGTTGCCACTCT 177

Qy   250 LeuCysAsnIleMetGlyPheProGlyProSerArgLeuAsnLeuHisPheThrVal 269
             |||       :::::       |||:::
Db   178 TTCTGCAACTACATGGGCCTTCCCTGCACTTCCAGTCGTGTGCACCCTGGAGCAT 225

Qy   270 AspLysLysAlaGlyArgIleSerLeuLysLeuValSerIleTrpAsn---LysCysTyr 287
             |||                    |||
Db   226 CCACAGAAGTGGGCCACTGCTGCACAGGCTATGCCTCGGGTGTGGGGAGACTTTTTCCTGCTTC 282
```

RESULT 3
US-10-646-950-1
; Sequence 1, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)

US-10-646-950-1

Alignment Scores:
Pred. No.:

Score: 2.86
Percent Similarity: 54.00
Best Local Similarity: 37.7%
Query Match: 24.6%
DB: 3.3%

Length: 1825
Matches: 75
Conservative: 40
Mismatches: 112
Indels: 80
Gaps: 15

US-10-646-950-4 (1-315) x US-10-646-950-1 (1-1825)

```
Qy     2 LeuGlnPheSerThrPheLeuValLeuLeuTyr---------IleSerIleSerTyrVal 18
             :::||||||       ||||||       :::
Db   130 TTAAACTTTTCCCTCTTTTTCACGTCAATTACTCAAAAAAACTTAATTCCTTCGTTCTCTG 189

Qy    19 LeuProLeuTyrAlaThrSerGlnProGlyGly--------SerLysArgAspAsnProArg 36
             :::                    |||       :::
Db   190 TTCTGCCATTTTCTCCAGAAAAAAAATCGACGGGAAATAAAAAAAGACAACGAACA 249

Qy    37                                         ThrIleLysSerArgMetGln 43
                                                     |||       |||
Db   250 GAGAAAAAGTTCCGGAATATATAAACCACTTCTTATAAATTAAACAGGAAAAGGAAGGAAAAAA 309

Qy    44 LysLeuThrIleMetLeuIleLeuSerAsnLeuPheLeuValProPheLeuGlnSerGlnLeu 63
```

Db   310 AAGGAGGAAGAAATAGAAAAACTGCAGGGCCTTATTCATGTTT------------------- 354
             ||| |||||||||||||||| |||
Qy   64 SerSerThrThrSerHis---------IleSerPheLys-AspAlaPheLeuGlyIleLeuGlyIl 81

Db   355 AAGACAGATTCTCGACCATTCCTAATATCCCGTGGAAATTAATCACATTTCTGGGT------ 406
             ::: ||| :::|| ||||||||||||
Qy   81 eIleProGlyTyrTyrAlaAlaLeuAlaLeuProAsnProTrpGlnPheSerGlnPheValLysAs 101

Db   407 --------------------------------TCTCGATTGCCCAAT------------- 432
             ||| |||
Qy   101 pLeu--------ThrLysCysValAlaAlaMetLeuLeuLeuThrLeuTyrCysGlyProValAla 118

Db   433 TCTTACTTGACGTACAGACAGTACCAGAAGCTACTCGAAACAAAAGTTGCCA--CCTGTGCT 491
             ||| ||| |||
Qy   118 GGAAGACGGAAATTGATGATGAAACTTTTCATAAAATCAAGGAGAACTACTCCCGGGCCCAAGGC 128

Db   492 GGAAGACGGAAATTGATGATGAAACTTTTCATAAAATCAAGGAGAACTACTCCCGGGCCCAAGGC 551
             ||| |||
Qy   128 oGlySerSerIleLeuGluAspPheTyrHisGluPheLeuAsnIleTrpSerPheArgAs 148

Db   552 CAAGTTCTTCCATTTTCGGGTGACGTCTAT---------AACCTTAGCCCAAAAAGCTAGT 599
             ::: |||
Qy   148 nPheIlePheAlaProIleThrGluGlnIleLeuPheTyrThrSerMetLeuLeuThrThrTy 168

Db   600 TTTCATCAAATACGACCTCTTCCCTAAAAATCTGGACACAGGCGGTTTCTTTA------- 651
             ||| |||
Qy   168 rLeuAsnLeuIleProHisSerGlnLeuSerTyrGlnLeuGlnLeuPheTrpGlnProSerIle 188

Db   652 -TTGAATGCAGT-CCTGCCAGTCAGATTTCATAT-------------- 683
             ||||||| ||:::   :::
Qy   188 uPhePheGlyLeuAlaHisAlaHisAlaTyrGluGlnLeuGlnGlyGlySerMetT 208

Db   684 --------GGTCTC------CACTGTCGCACAGAGTTTATTGCTTCTTGGGTCTCTTAT 727
             ::: |||
Qy   208 hrThrValSerIleLeuLeuThrThrCysPheGlnIleLeuLeuTyrThrThrLeuPheGlyG 228

Db   728 CCAGTTGTGTCTACCTTGGGTGAT----------TTGCCACTCTCTTACTATAGCCATTTGTCC 781
             ||| :::||
Qy   228 lyLeuThrLysPheValPheValArgThrGlyGlyAsnLeuTrpCysPheIlelleIleLeuLeuH 248

Db   782 TGGGAAGAAAAATTGGTTTCAATAAAATTGACCGTCCAACTATAGCAACACGGATATGATCA 841
             ||||||| :::::
Qy   248 isAlaLeuCysAsnIleMetGlyPheProGlyProSerArgLeuAsnLeuHisPheThrV 268

Db   842 AGAGTCTGACTTTGGCGTATGCTATTGGTGGGCCCAATC---CTTTTACCTGTTCCTTAAGA 898
             ||| |||
Qy   268 alValAspLys 271

Db   899 TCTTTGATAAA 909
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RESULT 4
US-10-646-950-3/c
; Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)

US-10-646-950-3

Alignment Scores:
Pred. No.:             3.17
Score:                 43.50
Percent Similarity:    37.5%
Best Local Similarity: 23.4%
Query Match:           2.6%
DB:                    1

Length:        2948
Matches:       45
Conservative:  27
Mismatches:    65
Indels:        56
Gaps:          10

US-10-646-950-4 (1-315) x US-10-646-950-3 (1-2948)

```
Qy     80 GlyIleIleProGlyTyr------------------------TyrAlaAlaLeuProAsn 91
          ||||||||:|||          ||:|:||||:::
Db   1903 GGTATCCTTCAGGGATATTAATCCAAAGGACCAGAGTGCGAAGTAGCACTTATTCCAGAT 1844

Qy     92 ProTrpGlnPhe--------------SerGln-PheValLysAspLeuThrLysCysValAlaMe 108
          ||::|                     ||:::
Db   1843 TCAGACCAAATTTGGAAAATGCGTCCAGCTTCTTGTCTACTACGTGAAATGTAAATTCAA 1784

Qy    108 tLeuLeuThrLeuTyrCysGlyProValLeuAspPheValLeuTyrHisLeuLeuAsnPr 128
          |||||                    ::||:|||
Db   1783 TCTTTGAA---------------------GGACCAGGAAACCCCATGATATTGCAAAGGGCATGCAGG-- 1738

Qy    128 oLySSerSerIleLeuGluAspPheTyrHisGluPheLeuAsnIleTrpSerPheArgAs 148
          |||||:|||                ::|
Db   1737 ----------ATTATGCAG----------CACCATAGGTTCCCGCCTGTTCTTACGAATACAAA 1694

Qy    148 nPheIlePheAlaProIleThrGluGlu-IlePheTyrThrSerMetLeuThrThrT 168
          :::|                    |||||:||||
Db   1693 CTTGGTTAACCCTCCAAAAAGTGTTGTGTATAAAATTTGGAAGCATGTTG----- 1644

Qy    168 yrIleuAsnLeuIleProHisSerGlnLeuSerTyrGlnGlnLeuPheTrpGlnProSerL 188
          ::::::|||||               |||||
Db   1643 -----------------------TCAGCAGAATGGAAACAGTTGTCATGGAGCCTTCCTG 1607

Qy    188 euPhePheGlyLeuAlaHisIleAlaHisHisAlaTyrGluGlnLeuGluGlnGlySerMetT 208
          ::|||||||                |||||:|||
Db   1606 TA--------------AATTGCTCATAAGCATGGTGCGGTGCCCAAGTCCAAAAAAAGCGATGG 1556

Qy    208 hr------------------------ThrValSerIleLeuLeuThr--------------- 215
          ||||||:::
Db   1555 TTGCCAAAATAACTGTTGATAGCTTAGTTGCGAATGCCGTATTAGGTTTAAGTACGTAGT 1496

Qy    216 --------------ThrCysPheGlnIleLeuThrThrLeuPheGlyLeuThrLysP 232
          ||||||                   |||
Db   1495 CAAAAGCAATTGACGTGTAA-AATATT------TCCTCAGTTATTGGGTGCAAATATAAAAT 1443

Qy    232 heValPheValArgThrGlyGlyAsnLeuTrp 242
          |||                      :::::|
Db   1442 TCCTGAAACTCCAAAATATTCAGGAATTCATGG 1411
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Search completed: April 18, 2006, 07:40:36
Job time : 2.64062 secs

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.7

Run on: April 18, 2006, 07:54:24 ; Search time 0.001 Seconds
                                            (without alignments)
                                            270.052 Million cell updates/sec

Title:
Perfect Score: 373
Sequence: 1 tttggagtcgcccatttca..........gcctcagagaccctactgtg 373

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 362 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 1 summaries

Database :   Pending_Patents_NA_Main:US-10-646-950-6

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21: /cgn2_6/ptodata/1/pna/US091_COMB.seq:US-10-646-950-6
22: /cgn2_6/ptodata/1/pna/US092_COMB.seq:US-10-646-950-6
23: /cgn2_6/ptodata/1/pna/US093_COMB.seq:US-10-646-950-6
24: /cgn2_6/ptodata/1/pna/US094_COMB.seq:US-10-646-950-6
25: /cgn2_6/ptodata/1/pna/US095A_COMB.seq:US-10-646-950-6
26: /cgn2_6/ptodata/1/pna/US095B_COMB.seq:US-10-646-950-6
27: /cgn2_6/ptodata/1/pna/US096A_COMB.seq:US-10-646-950-6
28: /cgn2_6/ptodata/1/pna/US096B_COMB.seq:US-10-646-950-6
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	13.6	3.6	362	54 US-10-646-950-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-6

; Sequence 6, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 6
; LENGTH: 362

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; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (93)..(156)
; OTHER INFORMATION: "n" is G, A, C or T
US-10-646-950-6

Query Match          3.6%;   Score 13.6;  DB 54;  Length 362;
Best Local Similarity   61.1%;
Matches   22;  Conservative   0;  Mismatches   14;  Indels   0;  Gaps   0;

Qy    277 TGCTTCTGCTTCAACCCCTGACAGACCCCAAGCTCT 312
          ||||  |||| |||  ||  ||    ||  |||||||
Db    324 TTCTCATCCTCCACTGCTAGAGAGAGACTTCAAGCTTT 359
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration ltd.

Run on: April 18, 2006, 07:49:48 ; Search time 1.01497 Seconds
                                                  (without alignments)
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Title: US-10-646-950-5
Perfect score: 373
Sequence: 1 tttggagtcgcccatttca..........gcctcagagacccactgtg 373

Scoring table: IDENTITY_NUC
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Database :   US10646950_1_3.seq:*
                Listing first 2 summaries

Post-processing: Minimum Match 0%
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 4

Searched: 2 seqs, 4773 residues

.Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
-1	30.5	8.2	2948	1	US-10-646-950-3	Sequence 3, Appli
2	16.4	4.4	1825	1	US-10-646-950-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-3
Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)
;
US-10-646-950-3

Query Match   8.2%;
Best Local Similarity   49.8%;
                                Score 30.5; DB 1; Length 2948;

Matches 102; Conservative   0; Mismatches 100; Indels   3; Gaps   1;

Qy   1 TTTGGAGTCGCCCATTTCACCACATTATTGAGCAGCTGCGCTTCCGCCAGAGACCCACTGTG 60
             ||||| ||||| ||| |||| ||| || || | || || || |||| ||| || |||
Db   1568 TTTGGACTTGCGCACGCACCACCATGCTTATTTATGAGCAATTACAGGAAGGCTCCATGACAACT 1627

Qy   61 GGAAGTACTTCGTTGTCTGCAGCGTTCCAGTTCTTCTCCTACACCGCGTGTCTTCGGTGCTTAT 120
             || || || ||| | | ||| || |||| || || |||| || || ||| || |||| ||
Db   1628 GTTTCCATTCTGCTGACAACACATGCTTCAAATTTATACACAACACTTTTTGGAGGTTA 1687

Qy   121 ACAGCTTTCCTCTTCATCCGCACA--GGACACCTGATAGGGCCGGTTCTCGCCACTCT 177
             || |||||| || |||| ||| || || ||| || || | ||| || || || ||
Db   1688 ACCAAGTTTGTATTCGTAAGAACAGGGCGGGAACCTATGGTGCTGCCATAATCCTCGCATGCC 1747

Qy   178 TTCTGCAACTACATGGGGCTTCCCTG 202
             ||| || ||| || | ||||||||
Db   1748 CTTTGCAATATCATGGGGGTTCCCTG 1772

RESULT 2
US-10-646-950-1
Sequence 1, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1825
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (343)..(1701)
;
US-10-646-950-1

Query Match   4.4%;
Best Local Similarity   45.4%;
Matches 59; Conservative   0; Mismatches 71; Indels   0; Gaps   0;
                                Score 16.4; DB 1; Length 1825;
                                Pred. No. 0;

Qy   98 ACACCGCTGTCTTCGGTGCTTATACAGCTTTCCTCTTCATCCGCACAGGACGACCTGATAG 157
             || | |||| || ||| | || || || || || || | ||| | || || |
Db   356 AGACGAATTCTCGACCATCCTAATATCCCGTGGAAATTAATCATTTCTTGGGTTCTCGATTG 415

Qy   158 GGCCGGTTCTCGCCACTCTTTCTGCAACTACATGGGGCTTCCCTGCAGTGTGTTCAGCGC 217
             || ||| || | ||| || | || || | || ||| | | || || |||| |
Db   416 CCCAATTTTCTTTCGAATCTTACTTGACGTACAGCACGTACCAGAAGCTATCTCGAAACAA 475

Qy   218 TGGAGCATCC 227
             |||| ||| |
Db   476 AGTTGCCACC 485

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration ltd.

Run on: April 18, 2006, 07:49:48 ; Search time 0.985034 Seconds
                                                  (without alignments)
                                                  3.508 Million cell updates/sec

Search completed: April 18, 2006, 07:49:50
Job time : 1.01497 secs

Title:
Perfect score: 358
Sequence: US-10-646-950-6
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Scoring table: IDENTITY NUC
                  Gapop 10.0 , Gapext 0.5

Searched: 2 seqs, 4773 residues

Total number of hits satisfying chosen parameters: 4

Database :   US10646950_1_3.seq:*

Post-processing: Minimum Match 0%
Maximum DB seq length: 0   Maximum Match 100%
Maximum DB seq length: 2000000000 Listing first 2 summaries

                             SUMMARIES

                    Query
Result
No.   Score   Match Length DB ID   Description
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c 1 33.7   9.4   1825   1   US-10-646-950-1   Sequence 1, Appli
   2 24.4   6.8   2948   1   US-10-646-950-3   Sequence 3, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                             ALIGNMENTS

RESULT 1
US-10-646-950-1
Sequence 1, Application US/10646950
GENERAL INFORMATION:
;   APPLICANT: Rine, Jasper
;   APPLICANT: Boyartchuk, Victor L
;   APPLICANT: Ashby, Matthew N
;   TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
;   FILE REFERENCE: B96-021-3
;   CURRENT APPLICATION NUMBER: US/10/646,950
;   CURRENT FILING DATE: 2003-08-21
;   PRIOR APPLICATION NUMBER: 60/023,491
;   PRIOR FILING DATE: 1996-08-07
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: Patentin Ver. 2.1
;
US-10-646-950-1
;   SEQ ID NO 1
;   LENGTH: 1825
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (343)..(1701)

Query Match   9.4%;   Score 33.7; DB 1; Length 1825;
Best Local Similarity   55.2%;   Conservative 0;   Mismatches 68; Indels 1; Gaps 1;
Matches 85;

Qy   196 TGAGTTTCAAGCTGATGCAT-TGCCAAGAAACTTGGGAAGGCTAAAGACTTATATTCTGC 254
          ||| ||||||||| | |||||||||| | ||| | |||| | | || ||| ||
Db   1509 TGAATATCAAGCTGATGCTTATCGTAAAAAATTCGGCTACAAGCAAAATCTATGTAGGGC 1568

Qy   255 TTTAATCAAAACTTAACAAAAGATAACTTGGGATTCCCTGTTTCTGACTGGTTGTTCTCAAT 314
          |||||||||||||| |||||||| ||| | |||||||||||| ||||||||||||
Db   1569 TCTAATTGATCTACAAAATCAAAATACCTTTCCACCATGAAATGTAGATCCTCTGTATTCTAG 1628

Qy   315 GTGGCCATTATTCTATCCTCCACTGCTAGAGAGA 348
          |||||||| | | |||||||||||||||||||
Db   [no db line shown]

Db   1629 CTATCATTATTCCATCCAACTCTAGCTGAAAGA 1662

RESULT 2
US-10-646-950-3/c
Sequence 3, Application US/10646950
GENERAL INFORMATION:
;   APPLICANT: Rine, Jasper
;   APPLICANT: Boyartchuk, Victor L
;   APPLICANT: Ashby, Matthew N
;   TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
;   FILE REFERENCE: B96-021-3
;   CURRENT APPLICATION NUMBER: US/10/646,950
;   CURRENT FILING DATE: 2003-08-21
;   PRIOR APPLICATION NUMBER: 60/023,491
;   PRIOR FILING DATE: 1996-08-07
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: Patentin Ver. 2.1
;
US-10-646-950-3
;   SEQ ID NO 3
;   LENGTH: 2948
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1001)..(1945)

Query Match   6.8%;   Score 24.4; DB 1; Length 2948;
Best Local Similarity   46.7%;   Pred. No. 0;   Mismatches 80; Indels 0; Gaps 0;
Matches 70;   Conservative 0;

Qy   27 TGTGTTTTTTTTTTTTATTTGCTGTATTTAATTGGTCGGAAAAGGAGACTTTTTGCTCGCATTTGGTT 86
          || |||| |||| || || | ||||| ||||| | |||||||| | | |||||||| |||
Db   2862 TATATTTTGTAAAGTATCTTGTACAAGCCTCTAGGAAATTATCAGGCTTAACGTTAGGGTG 2803

Qy   87 TTTATCNTAGCCAACCCACTNTATATTGNTCATCCTTCCAGTTTATTTTCAC 146
          ||||| || || ||| ||| || ||||| ||||||| | ||||||||
Db   2802 TTGATTGGGCGGAACCCATAATAAGTTTTTCTTTTAAATACGTTAGCATTTAATTTCCTGGA 2743

Qy   147 CTTACAATGNGGGTTCTTCTTTCTTTTTGCCTAA 176
          ||||||||| ||| ||||| |||||||||||||
Db   2742 TGGAGAGTGAACACCTTTTTTTATACCTAA 2713

Search completed: April 18, 2006, 07:49:50
Job time : 0.985034 secs

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OM protein - nucleic search, using frame_plus_p2n model

                        GenCore version 5.1.7
                        Copyright (c) 1993 - 2006 Bioceleration Ltd.

Run on:          April 18, 2006, 07:40:29 ; Search time 2.35938 Seconds
                        (without alignments)
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Title:           US-10-646-950-2
Perfect score:   2342
Sequence:        1 MFDLKTILDHPNIPWKLIIS..........HPTLAERSTALDYVSEKKKN 453

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Searched:        4 seqs, 5508 residues

Total number of hits satisfying chosen parameters:    8

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 4 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       US10646950.seq:*
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SUMMARIES

		%			
Result No.	Score	Match	Query Length	DB ID	Description
1	2342	100.0	1825	1	US-10-646-950-1	Sequence 1, Appli
2	194.5	8.3	362	1	US-10-646-950-6	Sequence 6, Appli
3	64	2.7	373	1	US-10-646-950-5	Sequence 5, Appli
c 4	61.5	2.6	2948	1	US-10-646-950-3	Sequence 3, Appli

ALIGNMENTS

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US-10-646-950-2 (1-453) x US-10-646-950-1 (1-1825)

Alignment Scores:
Pred. No.:                              5.22e-13
Score:                                  2342.00
Percent Similarity:                     100.0%
Best Local Similarity:                  100.0%
Query Match:                            100.0%

; US-10-646-950-1          Length:    1825
;                          Matches:    453
;                          Conservative:   0
;                          Mismatches:     0
;                          Indels:         0
;                          Gaps:           0
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Qy      1 MetPheAspLeuLysThrIleLeuAspHisProAsnIleProTrpLysLeuIleIleSer 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    343 ATGTTTGATCTTAAGACGATTCTCGACCATCCTAATATCCCGTGGAAATTAATCATTTCT 402

Qy     21 GlyPheSerIleAlaGlnPheSerPheGluSerTyrLeuThrTyrArgGlnTyrGlyLys 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    403 GGGTTCTCGATTGCCCAATTTTCTTTCGAATCTTACTTGACGTACAGACAGTACGGAAAG 462

Qy     41 LeuSerGluThrLysLeuValPheIleLysTyrAspLeuPheProLysIleLeuHisMetHis 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    463 CTAATCTGAAACAAAGTTGCCACCTGTCGCTGGAAAGACGAAAATTGATGAAGAACTTTCAT 522

Qy     61 LysSerArgAsnTyrSerArgAlaLysAlaLysPheGlyAspValTyrAsn 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    523 AAATCAAGGAACTACTCCCGGGCCAAGGCCAAGTTCGGTGACGTCTATAAC 582

Qy     81 LeuAlaGlnLysGlyLeuValPheIleLysSerTyrAspLeuPheProLysIleTrpHisMetAla 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    583 CTAGCCCAAAAGCTAGTTTTCATCAAATACGACCTCTTCCCTAAAATCTGGCACATGGCC 642

Qy    101 ValSerLeuLeuAsnAlaLeuValLeuProValArgPheHisMetValSerThrValAlaGln 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    643 GTTTCTCTTATTGAATGCACTAGTGCTCCTGCCAGTCAGATTCATATGGTCTCCACTGTCGGCACAG 702

Qy    121 SerLeuProPheLeuGlyLeuLeuSerSerLeuSerThrLeuValAspProLeuProLeuSer 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    703 AGTTTATTGCTTCTTGGGTCTCTTATCCAGTTTGTCTACCTTGGTTGATTTGCCACTCTCT 762

Qy    141 TyrTyrSerHisSerPheValLeuGluGluGlyLysPheGlyPheAsnLysHisLeuThrValGlnLeu 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    763 TACTATAGCCCATTTTGTCCTGGAAGAAGGAAAATTTGGTTCAATAAACATCACCTA 822

Qy    161 TrpIleThrAspMetIleLysSerLeuThrIleLeuAlaThrArgAlaIleGlyGlyProIleLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    823 TGGATCACCGATATGATCAAGAGTCTGACTATTTTGGCGTATCGAGCCATCGGTGGGCCAATCCTT 882

Qy    181 TyrLeuPheLeuLysIlePheAspGlyPheProThrAspPheLeuTrpTyrIleMetVal 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    883 TACCTGTTCCTTAAGATCTTTGATGGATTTCCTACTGATTTCCTTTGGTACATTATGGTC 942

Qy    201 PheLeuPheValValGlnIleLeuLeuValAlaMetThrIleIleProValPheIleMetProMet 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    943 TTCTTGTTCGTTGTCCAAATCTTAGCCATGACAATCATTCCAGTCTTCATCATGCCAATG 1002

Qy    221 PheAsnLysPheThrPheProLeuGluAspGlyGluLeuLysLysSerIleGlySerLeuAla 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1003 TTTAATAAGTTCACTCCATTCGGAGGACGGGTGAACTGAAAAAATCTATTGAAAGTTTGGCC 1062

Qy    241 AspArgValGlyPheProLeuLysIlePheValIleGluAspGlySerLysArgSerSer 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1063 GATAGAGGTTGGGGTTTCCCTCTGAAGATAGATTTTTGTCATTGACGGGCTCAAAAAGATCTTCT 1122
```

RESULT 2

```
US-10-646-950-6
Sequence 6, Application US/10646950
GENERAL INFORMATION:
 APPLICANT: Rine, Jasper
 APPLICANT: Boyartchuk, Victor L
 APPLICANT: Ashby, Matthew N
 TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
 FILE REFERENCE: B96-021-3
 CURRENT APPLICATION NUMBER: US/10/646,950
 CURRENT FILING DATE: 2003-08-21
 PRIOR APPLICATION NUMBER: 60/023,491
 PRIOR FILING DATE: 1996-08-07
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 6
 LENGTH: 362
 TYPE: DNA
 ORGANISM: human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (93)..(156)
 OTHER INFORMATION: "n" is G, A, C or T
```

Alignment Scores:

Pred. No.:	0.651
Score:	194.50
Percent Similarity:	52.2%
Best Local Similarity:	36.6%
Query Match:	8.3%

Length:	362	Matches:	49
		Conservative:	21
		Mismatches:	49
		Indels:	16
		Gaps:	2

US-10-646-950-6 (1-453) x US-10-646-950-6 (1-362)

```
Qy  261 HisSerAsnAlaTyrPheThrGlyLeuProPheThrSerLysArgIleValLeuPheAsp 280
        |||||
Db 1123 CATTCAAACGCATATTCACAGGTTTGCCATTCACCTCAAAGAGAATTGTTTTGTTTGAC 1182

Qy  281 ThrLeuValAsnSerAsnSerThrAspGluIleIleThrAlaValLeuAlaHisGluIleGly 300
        |||||
Db 1183 ACTTTAGTGAACAGTAATTCTACTGATGAAATTACGGCGTTTTGGCCCATGAAATCGGT 1242

Qy  301 HisTrpGlnLysAsnHisIleVAlAsnMetValIlePheSerGlnLeuHisThrPheLeu 320
        |||||
Db 1243 CACTGGCAAAAAAACCACATCGTTAAATATGGTCATCTTTAGTCAAATTGCACACCTTCCTC 1302

Qy  321 IlePheSerLeuPheThrSerIleTyrArgAsnThrSerPheThrTyrAsnThrPheGlyPhe 340
        |||||
Db 1303 ATTTTCTCCCTTTTCACCAGCACTCTACAGAAATACATCATTTACAACACCTTCGGCTTT 1362

Qy  341 PheLeuGluLysSerThrGlySerPheValAspProValIleIleThrLysGluPheProIle 360
        |||||
Db 1363 TTCTTAGAAAAGTCCACTGGCAGTTTTGTTGATCCGGTTATCATAACTAAGGAATTCCCCATT 1422

Qy  361 IleIleGlyPheMetLeuPheAsnAspLeuLeuThrProLeuGluCysAlaMetGlnPhe 380
        |||||
Db 1423 ATCATTGGATTAATGTTATTTAACGACTTATTAACTCCACTCGGATGTGCCATGCAATTC 1482

Qy  381 ValMetSerLeuLeuSerArgThrHisGluTyrGlnAlaAspAlaTyrAlaLysLysLeu 400
        |||||
Db 1483 GTGATGAGTTTATTTCAAGCAGATGCTTATGCTAAAAAATTG 1542

Qy  401 GlyTyrTyrLysGlnAsnLeuCysArgAlaLeuIleLeuAspLeuGlnIleLysAsnLeuSerThr 420
        |||||
Db 1543 GGCTACTACAAGCAAAATCTATGTAGGGCTCTAATTGACCTTCAAATCAAAAACCTTTCCACC 1602

Qy  421 MetAsnValAlaSerProLeuTyrSerSerTyrHisTyrSerHisProThrLeuAlaGluArg 440
        |||||
Db 1603 ATGAATGTAGCATCCCTCTGTATTCTAGCTATCATTATCCCATCCAAACTCTAGCTGAAAGA 1662

Qy  441 SerThrAlaLeuAspTyrValSerGlyLeuLysLysLysAsn 453
        |||||
Db 1663 TCGACCGCTCTAGACTATGTTAGTGAAAAGAAAGAAAAC 1701
```

RESULT 3

```
US-10-646-950-5
Sequence 5, Application US/10646950
GENERAL INFORMATION:
 APPLICANT: Rine, Jasper
 APPLICANT: Boyartchuk, Victor L
 APPLICANT: Ashby, Matthew N
 TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
 FILE REFERENCE: B96-021-3
 CURRENT APPLICATION NUMBER: US/10/646,950
 CURRENT FILING DATE: 2003-08-21
 PRIOR APPLICATION NUMBER: 60/023,491
 PRIOR FILING DATE: 1996-08-07
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 5
 LENGTH: 373
 TYPE: DNA
 ORGANISM: mouse
```

Alignment Scores:

Pred. No.:	2.89
Score:	64.00
Percent Similarity:	40.5%
Best Local Similarity:	25.3%
Query Match:	2.7%

Length:	373	Matches:	20
		Conservative:	12
		Mismatches:	37
		Indels:	10
		Gaps:	2

US-10-646-950-2 (1-453) x US-10-646-950-5 (1-373)

```
Qy  299 IleGlyHisTrpGlnLysAsnHisIleVAlAsnMetValIlePheSerGlnLeuHisThr 318
        ::: |||||::: :::|||:::|  :::
Db   61 GGAAGTATATCTTCGTTGTCTGCAGGCGTTCCAGTTCTCTACACCGCTCTCTCGGTGTCTAT 120

Qy  319 PheLeuIlePheSerLeuPheThrSerIleTyrArgAsnThrSerPheThrTyrAsnThrPhe 338
        |||||::: :::
Db  121 ACAGCTTTCTTCTTCAGCAGACACCTGAGATAGGGCGCGGTTCTCTGCACTCGTTTC 180
```

```
Qy   359  ProIleIleGlyPheMetLeuPheAsnAspLeuLeuThrProLeuGluCysAla 377
                        :::|||||
Db   181  TGCAACTACATGGGCTTC------------------CCTGCAGTGTGTGCA 213
```

US-10-646-950-3/c

RESULT 4
GENERAL INFORMATION:
  Sequence 3, Application US/10646950
  APPLICANT: Rine, Jasper
  APPLICANT: Boyartchuk, Victor L
  APPLICANT: Ashby, Matthew N
  TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
  FILE REFERENCE: B96-021-3
  CURRENT APPLICATION NUMBER: US/10/646,950
  CURRENT FILING DATE: 2003-08-21
  PRIOR APPLICATION NUMBER: 60/023,491
  PRIOR FILING DATE: 1996-08-07
  NUMBER OF SEQ ID NOS: 6
  SOFTWARE: PatentIn Ver. 2.1
  SEQ ID NO 3
    LENGTH: 2948
    TYPE: DNA
    ORGANISM: Saccharomyces cerevisiae
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1001)..(1945)
US-10-646-950-3

Alignment Scores:

Pred. No.:	2.96	Length: 2948
Score:	61.50	Matches: 68
Percent Similarity:	38.2%	Conservative: 56
Best Local Similarity:	20.9%	Mismatches: 108
Query Match:	2.6%	Indels: 93
DB:	1	Gaps: 15

US-10-646-950-2 (1-453) x US-10-646-950-3 (1-2948)

```
Qy    18  IleIleSerGlyPheSerIleAlaGlnPheSerPheGluSerTyrLeuThr-TyrArgGl  37
                   |:::|||||
Db   860  ATCATCAAAGGTTTCCATCCAGTGGTCCAAAAAAAAAAAATACAGAGAGCAACAAAAGA 801

Qy    37  nTyrGlnLysSerGluThrLysLeuProProValLeu---------GluAspGlu1l  54
                   :::||||||:::
Db   800  GCACCAGAAAATGCATTTAAAAGAATTTTATTAATATAGGGAATACAAAGGACCGGAT 741

Qy    54  eAsp------------------AspGluThrPheHisGlySer------ArgAsnTyrSerAr  67
                   |:::
Db   740  AAATACCTTCATCTATTAAGCAACCATACATATTCTATACTGTATAAGAAAAGTAACGAG 681

Qy    67  gAlaLysAlaLysPheSerIlePheGlyAspValTyr------------------  79
                   :::|||||:::
Db   680  A------ATTTTTCTAAGTTTTTATTTTATTTGTTCACTTGCCTAACACAG 639

Qy    80  ------AsnLeuAlaGlyLeuValPheIleLeuValTyrAspLeuPhePro-  94
                   |||
Db   638  AAATAGGGATATCAATCTTCGCTACGCCAAGATGGTTTTCAAATTTAATTCATTACTCGAA 579

Qy    95  --------------------LysIleTrpHisMetAlaValSerLeuuLe 104
Db   578  CGCAATAAAACCTACAACATAGGCAGCTTTCAAAACTTGGAAT------TAAAGTTTCCT 525

Qy   104  uAsnLeuAlaValLeuProValArgPheHis-MetValSerThrValAlaGlnSerLeuCysP 124
                   ||||:::
Db   524  TAAGTCCTTATTAAATTCCAAGTTCACATTAAGTGTCTCGTTTG------TACTGTA 474

Qy   124  heLeuGlyLeuLeuSerSerLeuSerThrLeu----------------- ValAsp- 136
                   :::||||||:::
Db   473  AAGGAGCAACCTACCATTATGAACAACTCGGTCTGTAAATTCAGGAGGAAGTAGACG 414

Qy   137  --LeuProLeuSerTyrTyrSerHisPheValLeuGluGluLysPheAsnLysL 156
                   :::
Db   413  AGCTACCGCTAGGTAAAAATAAACTACTCTTGGATGAAGAAGTTACTGGCGGTTAATGACG 354
```

```
Qy   156  eu------------------------ThrValGlnLeuTrpIleThrAspMetIleLysSerLeuThrL 171
Db

Qy   353  CTGAAACTGGGCGACGATGAACATACCGTTACCCTGTGTGCCGATAATTGAAATCCTCAGATAAG 294
                   :::
Db   293  CGTGCTTGAGTGTGTTGTTTTAGGTACTGACCTGTGTTTTTAAAAATGTTGGAATAAGTTGT 234

Qy   171  euAlaTyrAlaIleGlyPheIleLeuLeuTyrIleLeuPheLeuLeuLysIlePheAspProLeu 191
Db

Qy   191  roThrAspPheLeuTrpTyrIleMetValPheLeuuValGlnIleuLeuLeuAlaMetT 211
Db   233  GAACA

Qy   211  hrIleLeuProValPheIleMetProMetPheAsnLysPheThrProLeuGluAspGlyG 231
Db   197  CG------                                        TTAAACAGCTGTG 183

Qy   231  lLeuLysLysSerIleGluSerLeuAlaAspArgValGlyPheProLeuAspLysIleP 251
Db   182  AAGTAATAAAATCTGTAAATTCAGTTCCTTGGCCTAACGAGTCCCTA---                T 132

Qy   251  heValIleuAspGlySerLysArgSer-----------------            SerHisSerA 263
                   ||:::::
Db   131  TCATATTATATAACTCATTAATTCAAGAAAAATTCTTGTTGAACTTGGTTTCAATATTCAC 72

Qy   263  snAlaTyrPheThrGlyLeuProPheThrSerLysArgIleuValLeuuPheAspThrLeuV 283
Db    71  AAATTTTTGAATGTGAAATCATCCTACAAAAGCGTTTGATGCGTTGTTCGTCAGCTTCTCTTTTGTTCA 12

Qy   283  alAsnSerAsn 286
                   :::||||||:::
Db    11  TCAACAGTTCA 1
```

Search completed: April 18, 2006, 07:40:35
Job time : 4.35938 secs

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 18, 2006, 07:40:29 ; Search time 1.64062 Seconds
                                            (without alignments)
                                            2.115 Million cell updates/sec

Title: US-10-646-950-4
Perfect score: 1651
Sequence: 1 MLQFSTFLVLLIYISISYVLP..........ISLKDTLQTLVGTPGYRITL 315

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop   6.0 , Fgapext   7.0
                Delop   6.0 , Delext   7.0

Searched: 4 seqs, 5508 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 4 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=soft -Q=US10646950.pep -DB=US10646950.pep
-SUFFIX=pto -OUT=align_p2n -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=4 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=4 -MODE=LOCAL -OUTFMT=pto

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-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000000 -NCPU=6 -NO_XLPXY
-NBG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Database :　　US10646950.seq:*

Pred. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	% Length	DB	ID	Description
1	1651	100.0	2948	1	US-10-646-950-3	Sequence 3, Appli
2	163	9.9	373	1	US-10-646-950-5	Sequence 5, Appli
3	54	3.3	1825	1	US-10-646-950-1	Sequence 1, Appli
4	43.5	2.6	2948	1	US-10-646-950-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-646-950-3
; Sequence 3, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2948
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1001)..(1945)

US-10-646-950-3

Alignment Scores:
Pred. No.:　　　　　3.08e-09
Score:　　　　　　　1651.00
Percent Similarity:　100.0%
Best Local Similarity:　100.0%
Query Match:　　　　100.0%
DB:　　　　　　　　1

Length:　　2948
Matches:　　315
Conservative:　0
Mismatches:　0
Indels:　0
Gaps:　0

US-10-646-950-4 (1-315) x US-10-646-950-3 (1-2948)

Qy   1 MetLeuGlnPheSerThrPheLeuValLeuTyrIleSerTyrValLeuPro 20
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1001 ATGCTACAAATTCTCAAACATTTCTAGTGCGTTCCTATACATCTCATAYGTGCTACCG 1060

Qy   21 LeuTyrIleAlaThrSerGlnProGlyGlySerLysArgAspAsnProArgThrIleLysSer 40
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1061 CTATATGCAAACTTCACACCAGAAGGGGTCTAAACGAGATAAATCCTCGAACGGATTAAAATCT 1120

Qy   41 ArgMetGlnLysGluLeuThrIleMetLeuIleSerAsnLeuPheLeuValProPheLeuGln 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1121 CGCATGCAAAAACTTACAATTATGCTAATTTCCAACCTTTTTGGTGCCTTTTTACA 1180

Qy   61 SerGlnLeuSerThrThrSerHisIleSerPheLeuTyrAspAlaPheLeuGlyLeuGly 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1181 TCTCAATTATTCTAGTACCAACTTCACATATAAGTTCAAGGACGGCATTTTTAGGCTTAGGT 1240

Qy   81 IleIleProGlyTyrTyrAlaAlaLeuAlaLeuProAsnProTrpGlnPheSerGlnPheValLys 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1241 ATTATCCCAGGTTATTACGGTGCATTGGCAATAAACCCTTGGCAATTCAGCCAGTTCGTGAAA 1300

Qy 101 AspLeuThrLysCysValAlaMetLeuLeuLeuThrLeuTyrCysGlyProValLeuAspPhe 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1301 GACTTAACGAAATGYGTTGCCATGYTATTGCTAACGTTATATGTGGACCCGGTTTAGATTTT 1360

Qy 121 ValLeuTyrHisLeuLeuAsnProLysSerSerIleLeuGluAspPheTyrHisGluPhe 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1361 GTAATATATCATTTATTAAATCCAAAGAGCTCTATACTTGAAGATTTTTACCATGAATTC 1420

Qy 141 GlnLeuPheTrpGlnProSerLeuPhePheGlyLeuAlaHisSAlaHisHisSAlaTyrGlu 160
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1421 CAGTTGATTTGGCAACCATCGCTTTTTTTGGACTTGCGGCACCGCACCATTGCTTATGAG 1480

Qy 161 ThrSerMetLeuLeuThrThrTyrLeuAsnLeuIleProHisSerGlnLeuSerTyrGln 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1481 ACGTCAATGCTTTTGACTACGTACTTAAACCTAATACCGCATTCGCAACTAAGCTATCAA 1540

Qy 181 LeuAsnIleLeuTrpSerPheAsnArgAsnPheIleThrValSerIleLeuLeuLeuThrCysSPheGluIle 200
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1541 CTTGAATATTTGGAGTTTCAGGAATTTATAAATTTTGCACCAATAACTAACGAAAATATTTTAC 1600

Qy 201 GlnLeuGlnLeuGlyLySerMetThrThrValSerIleLeuIleLeuLeuThrThrCysPheGlyIleLeu 220
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1601 CAATTACAGGAAAGGCTCCATGACAACCGTTTCCAATCTGCTGACAACATGGTTCCAAATT 1660

Qy 221 LeuTyrThrThrLeuPheGlyGlyLeuThrLysPheValPheValArgThrGlyGlyAsn 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1661 TTATACACAACACTTTTTGGAGGTTTAACCAAGTTTGTAATTCGTAGGACACGAGGCGGGAAC 1720

Qy 241 LeuTrpCysGlySIleIleLeuGluHisSAlaLeuCysAsnIleMetGlyPheProGlyProSer 260
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1721 CTATGGTGTGGCATAATCCTCGAACATGCCCTTGCCAATATCATGGGGTTTCCTGGTCCTTCA 1780

Qy 261 ArgLeuAsnLeuHisPheThrValAlaSpLysLysAlaGlyArgIleSerLysLeuVal 280
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1781 AGATTGAAATTACATTTCACAGTAGCAGACAAGAAAGCTCGGAACGCGATTTCAAAATGGTC 1840

Qy 281 SerIleLeuTrpAsnLysCysTyrPheAlaLeuLeuLeuValLeuGlyLeuIleSerLeuLysSAsp 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1841 TCAATCTGGAATAAGTGCTACTTCGCACTGCTGGTCCTTGGATTAATATCCCTGAAGGAT 1900

Qy 301 ThrLeuGlnThrLeuValGlyThrProGlyTyrArgIleThrLeu 315
         |||||||||||||||||||||||||||||||||||||||||||
Db 1901 ACCTTACAAAACTCTCGGTAGGAACTCCCTGGTTATAGAAATAAACCCTT 1945
```

RESULT 2
US-10-646-950-5
; Sequence 5, Application US/10646950
; GENERAL INFORMATION:
; APPLICANT: Rine, Jasper
; APPLICANT: Boyartchuk, Victor L
; APPLICANT: Ashby, Matthew N
; TITLE OF INVENTION: AFC1 and RCE1: Isoprenylated CAAX Processing Enzymes
; FILE REFERENCE: B96-021-3
; CURRENT APPLICATION NUMBER: US/10/646,950
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: 60/023,491
; PRIOR FILING DATE: 1996-08-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 373
; TYPE: DNA
; ORGANISM: mouse

US-10-646-950-5

Alignment Scores:
Pred. No.:　　　　　0.831
Score:　　　　　　　163.00
Percent Similarity:　54.5%

Length:　　373
Matches:　　36
Conservative:　18